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# Intrinsic circular motions in stochastic pairwise epidemic models

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## HIGHLIGHTS

- A pairwise SIS epidemic model with moment closure is studied.
- Circular motion is discovered, showing the non-equilibrium property of the model.
- These circular motions exist both in the diffusion process and in the discrete process.
- In the diffusion process, it is characterized by the imaginary eigenvalues of the covariance matrix.
- In the discrete process, it is characterized by the cross-correlations.

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## ABSTRACT

The main purpose of the paper is to show that there exists intrinsically stochastic circular motion in a pairwise epidemic model, which does not exist in the classical mean-field susceptible–infective–susceptible (SIS) models. Here a basic pairwise SIS epidemic model is adopted. By the method of scale-separation in the case of a large population, we can get a deterministic dynamical system—which represents the temporal evolution of averaged densities of the system; plus a diffusion process, which is centered at the orbit of the aforementioned deterministic system. It is discovered that there is a mode of circular motion in the diffusion process. We consider that this intrinsic circular motion must originate from the fact that the original stochastic pairwise process is time irreversible, since the intrinsic periods, which are calculated from the two systems respectively, have similar forms.



## 1. Introduction

On the level of individual hosts, the propagation of disease is essentially discrete and stochastic [1]. Though early models in epidemiology were largely deterministic, each of them can be viewed as a macroscopic approximation of an underlying stochastic mesoscopic model. Generally, stochastic models produce more information than deterministic ones. For example, it has been reviewed that noise may play fundamental roles in epidemic dynamics [2,3], such as the sustaining of damped cycles [4], the amplification of demographic stochasticity [5], and the dynamical resonances [6] and so on.

On understanding the cause(s) of the often observed noisy oscillations (fluctuations) in epidemiological data [7], models in deterministic framework focus mainly on an interacting between external forces and inherent frequencies in a nonlinear dynamics [8], while stochastic models can illustrate the fundamental role of intrinsic randomness [3,6,9].

In studying the basic susceptible-infectious-susceptible (SIS) epidemics, the classical models are based on the mean-field assumption, i.e. individuals are all homogeneous and well-mixed [10]. There is no oscillatory dynamics in these classical

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models: neither in deterministic ones nor in stochastic ones. In the former, there exist at most two attracting equilibrium states: a trivial stable "node" or a non-trivial stable "node". And the stochastic SIS model is just a one-dimensional birth-and-death process [11,12], it is well-known that the stationary distribution of a one-dimensional birth-and-death process is unique, if it exists; and the stationary process is time reversible, which means there is no circular motion in this process.

Mean-field models are only the zeroth approximation of the realistic disease propagation. In some cases such as the sexually transmitted diseases, spatial structure and correlation play fundamental roles in disease propagation. In order to address these factors in a model while keeping it still tractable and controllable, pairwise models have been developed and many new phenomena found [2,13–16].

In this paper, using the basic pairwise model [2,14,16], we show that there is another intrinsic property in this class of models, which will never emerge in the classical mean-field models. By adopting the so-called big $\Omega$-expansion method in the case of large population size [17], we get a deterministic dynamical system which represents the temporal evolution of the macroscopic "densities" [3], and a linear diffusion process which is centered at the orbit of the former system. The deterministic dynamical system is studied clearly in the literature [14]—there exists only one type of steady state: the globally stable "node", trivial or non-trivial under different parametric conditions, thus there is no periodic orbit at all. Whereas we will show in this paper that there exist circular motions in the diffusion process which are centered at the non-trivial stable "node" of the deterministic system. We think this new discovery provides new insights into the understanding of the periodic fluctuations observed in epidemiological data.

The remainder of the paper is organized as follows. In Section 2, we introduce the stochastic pairwise model, which can be seen as a birth-and-death process in two-dimensional lattice space. In Section 3, we analyze the intrinsic circular motion in the diffusion process, and show the existence of circular motion in the original stochastic pairwise process. The dependences of the intrinsic frequency (period) on the transition parameter $\lambda$ are calculated for both systems. It is interesting that the curves are closely similar, which suggests to us that the origin of the intrinsic circular motion is time asymmetric in the original stochastic pairwise model. And in Section 4 there is the conclusion.

## 2. The pairwise model

Firstly let us give a brief introduction to the basic SIS model. Here it is supposed that the whole population consists of $N$ individuals, every one has $k$ neighbors, and every one is in one of two states: susceptible (denoted by S) or infectious (I).

Almost all classical epidemic models are based on the mass action principle (in another word, mean-field assumption), i.e. individuals are assumed to be homogeneous and well mixed. Under this assumption, the intensity of a susceptible individual to be infected is proportional to the density of infectious individuals: $\lambda N_I/N$. Here $N_S$ and $N_I$ denote the number of two individual types respectively, with the conservation $N_S + N_I = N$; and $\lambda$ denotes the transmission intensity of a "collision" (or contact). On the other hand, an infectious individual will recover after an exponentially distributed dwell time—the parameter of which has been normalized to be unity. Assuming that two kinds of fundamental stochastic events: the collisions of two individuals and the recovering of infectious, are all independent, one can characterize this stochastic demographic process through a birth-and-death process $\{N_I(t); t \in [0, +\infty)\}$ in the bounded one-dimensional lattice $[0, N] \cap Z^1$, with the following types of transitions and corresponding rates:

$$n-1 \underset{n}{\overset{\lambda(N-n+1)\frac{n-1}{N}}{\rightleftharpoons}} n \underset{n+1}{\overset{\lambda(N-n)\frac{n}{N}}{\rightleftharpoons}} n+1. \tag{2.1}$$

Here $n$ is a point in the state space. And note that the recovery rate of a single infectious individual is unity, since the dwell time distribution is parameterized to be unity. Obviously, the state 0 is an absorbing state and the unique stationary distribution of this process is a degenerate one at 0.

To study the more informative dynamics in the pre-extinction phase, one method is the quasi-stationary approximation [12]. Here we introduce a very tiny transition probability $\epsilon \ll 1$, representing that the process can "return from" the state 0, thus abolishing the absorbing state. Since the state space is finite and irreducible, there exists a unique stationary distribution. Biologically, $\epsilon$ can be interpreted as an infinitesimal invasion by migration or recurrence of infectious individuals. The transition at state 0 now becomes:

$$0 \underset{1}{\overset{\epsilon}{\rightleftharpoons}} 1. \tag{2.2}$$

Let $P(n; t) = \mathrm{Prob}(N_I(t) = n)$, we can write the temporal evolution of the probability distribution, the so called master equation (or Kolmogorov forward equation):

$$\begin{aligned}
&\frac{\mathrm{d}P(N;t)}{\mathrm{d}t} = \lambda\frac{N-1}{N}P(N-1;t) - NP(N;t);\\
&\frac{\mathrm{d}P(n;t)}{\mathrm{d}t} = \lambda(N-n+1)\frac{n-1}{N}P(n-1;t) + (n+1)P(n+1;t) - \left[\lambda(N-n)\frac{n}{N} + n\right]P(n;t); \quad 1 \le n < N\\
&\frac{\mathrm{d}P(0;t)}{\mathrm{d}t} = P(1,t) - \epsilon P(0,t).
\end{aligned} \tag{2.3}$$